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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd. OM protein - protein search, using sw model

March 2, 2006, 04:10:57 ; Search time 185 Seconds
(without alignments)
121.126 Million cell updates/sec Run on:

51

1 MLQMAGQCSQNEYFDSLLHA......TPPLTCQRYCNASVTNSVKG

Sequence:

US-10-077-438-1\_COPY\_1\_51 51 Title: Perfect score:

<u>ලාණි</u>ලය Gapop 60.0 , Gapext 60.0 යුගෙන්ගල <del>අ</del>බෝලෘ

2443163 seqs, 439378781 residues Searched:

• अंटाइटी इधियन १

Total number of hits satisfying chosen parameters:

2443163

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Listing first 45

Genesed Database :

geneseqp2003as: geneseqp1980s:\* geneseqp2005s:\* geneseqp2000s: geneseqp2002s: geneseqp2003bs geneseqp2004s: geneseqp2001s: geneseqp1990s

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aec02032 Amino aci	Aab08843 Amino aci	Aay94001 A human B		Aay71979 Human B c	Aab60698 Human BAF	Aae00506 Human B c	Abb81487 Human BCM	Abp54694 Metastati	Aae28961 Human B-c	Aae35216 Human B-c	Ada49361 Human BCM		Abp97717 Amino aci	Add67527 Human Ly1		Adk00756 Native hu	Adq94442 Neutrokin	Adp56014 Human PRO	Adw03432 Human BCM	Adz67760 Human tum	Tumo	Aec02031 Amin acid	Aab60699 Mouse IgG
SUMMARIES	ΔΙ	AEC02032	AAB08843	AAY94001	AAE09241	AAY71979	AAB60698	AAE00506	ABB81487	ABP54694	AAE28961	AAE35216	ADA49361	ABP60552	ABP97717	ADD67527	ADG43715	ADK00756	ADQ94442	ADP56014	ADW03432	ADZ67760	AEA23348	AEC02031	AAB60699
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## ALIGNMENTS

AEC02032 standard; peptide; 52 AA. RESULT 1 AEC02032 

AEC02032;

20-OCT-2005 (first entry)

Amino acid sequence of an extracellular domain of BCMA

APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer; cytostatic; neoplasm; immunosuppressive; therapeutic; B-cell maturation antigen; BCMA.

Synthetic.

WO2005075511-A1

18-AUG-2005.

04-AUG-2004; 2004WO-US025247.

29-JAN-2004; 2004US-0540271P.

(GETH ) GENENTECH INC.

Kelley RF, Patel D;

WPI; 2005-555932/56.

New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, usefu for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation.

Disclosure; SEQ ID NO 21; 140pp; English.

The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematoeus; cancer such as leukemia, lymphoma, or multiple scleroms or T-cell mediated disease such as graft rejection, graft versus host disease (GYHD) and inflammation. The present sequence

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Gaps

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Indels

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0; Mismatches

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51; Conservative
 Matches
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                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                               BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
                                                                      Gaps
                                                                                                         1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                              1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                   Length 52;
                                                                      Indels
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57. 77
/note= "putative transmembrane domain"
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                                   100.0%; Score 51; DB 9; I
100.0%; Pred. No. 1.4e-47;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                    AAB08843 standard; peptide; 184 AA
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                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of human.
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                                      Query Match
Best Local Similarity
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     Sequence 52 AA;
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                                                                            Matches
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Score 51; DB 3; Length 184; Pred. No. 4.1e-47;

100.0%;

Query Match Best Local Similarity

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The present sequence represents a human BCMA protein, a B cell protein crelated to transmembrane activator and CAML-interactor (TACI) receptor.

Taci is a tumour necrosis factor (TNF) receptor. The extracellular command is soften of TACI). TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting zthf4 activity. Zthf4 is a TNF ligand. They may also be used for inhibiting sthf4 activity. Zthf4 is a TNF ligand. They may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an automatory and BR43x2. TACI or BCMA receptor-ligand enthritis. The zthf4 activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with a sethma, bronchitis, emphysema, end stage renal failure, and stage renal failure, companies, multiple myelomas, lymphomas, light chain neuropathy, completion, graft versus host disease, inflammation, insulin dependent comparities, or septic shock. BR43x2, TACI, and BCMA polypebtides, fusions, antibodies, septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, companies or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli
                                                                                                                                                                                                                                                                                                                                   Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; ztnf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                 A human BCMA protein, a B cell protein related to TACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 152; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yee DP;
                                                                                                                                                                 AAY94001 standard; protein; 184 AA.
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                                                                                                                                                                                                                                                           20-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-452538/39.
N-PSDB; AAA58559.
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                                                                                                                                                                                                               AAY94001;
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Human B cell maturation factor (BCMA) protein.

(first entry)

28-MAR-2001 AAY71979;

AAY71979 standard; protein; 184 AA.

RESULT 5 AAY71979

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The present sequence is human BCMA protein
                                                                                                                                                                                                                                                                                                                                                                                           TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, ARIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and ARIL expression or
                                                                                                                                                                                                                                                                                                                                                                          TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                       1 MLQMAGQCSQNEYFDSLLHACIPCQRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                               1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                            Length 184;
                                                                               0; Indels
                                             Score 51; DB 3; I
Pred. No. 4.1e-47;
                                                                               0; Mismatches
                                                                                                                                                                                                                                   AAE09241 standard; protein; 184 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-FEB-2000; 2000US-0182938P.
22-AUG-2000; 2000US-0226986P.
                                             / Match 100.0%;
Local Similarity 100.0%;
les 51; Conservative 0
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                                                                                                                                                                                                                                                                                                                                        Human BCMA protein.
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                 Sequence 184 AA;
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related Leucocyte expressed Ligand 1 (FALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate moncoyte, macrophage and B lymphocyte mediated immune responses. CC TALL-1 protein is useful for identifying compounds that regulate B compounds that regulate B cc lymphocyte profileration. It is also useful for treating B lymphocyte asponses. CC special autoimmune disorders like rheumatoid arthritis, systemic lupus crythematosus (SLE), insulin dependent diabetes mellitus, multiple crythematosus (SLE), insulin dependent diabetes autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal corresponding nucleic acid sequence are also useful in diagnostic assays. The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is the receptor for TALL-1 protein. BCMA gene is located on chromosome In human tissues, BCMA is expressed by spleen and lymph nodes but not reain, muscle, heart, lung, kidney, pancreas, testis and placenta. In the pro-B lymphocyte stage but its expression eases with B lymphocyte maturation
                                                                                                                                       Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
Therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
haemolytic anaemia, Grave's disease; myasthenia gravis; chromosome 16;
post streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention relates to Tumour necrosis factor (TNF) and ApoL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.

    .62
    /label= Extracellular_domain

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                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-2000; 2000WO-US012266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000; 2000US-0201012P
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BCMA mRNA is absent in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-016094/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1999;
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Sequence 184 AA;

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Gaps

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0; Indels

100.0%; Score 51; DB 4; Length 184; 100.0%; Pred. No. 4.1e-47;

100.0%; Pred. ....

51; Conservative

Query Match Best Local Similarity

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1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51

1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51

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Gaps

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0; Indels

0; Mismatches

100.0%; Score 51; DB 4; Length 184; 100.0%; Pred. No. 4.1e-47;

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Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapid progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents human BAFF-R
                                                                                                                                                                                                                                                                                                                                                              1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                              1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour.
                                                                    Gaps
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0
                                                                                                                                                               1 MLQMAGQCSQNEYFDSLLHACTPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                   1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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         Length 184;
                                                                 Indels
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0
                                        4.1e-47;
            Score 51; DB 4;
Pred. No. 4.1e-47
                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                               AAB60698 standard; protein; 184 AA.
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            100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0181684P
2000US-0183536P
                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human BAFF receptor (BAFF-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                        51; Conservative
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            Query Match
Best Local Similarity
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11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                          AAB60698;
                                                                           Matches
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The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lupus erythematosus-SLB); hypertension, cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
                                                                                                       Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus exythematosus; ELF; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; tumour necrosis factor; BCMA; B cell maturation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating a mammal for a condition associated with undesired cell
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                                                                           Human B cell maturation protein (BCMA).
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                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-1999; 99US-0157933P.
11-FEB-2000; 2000US-0181807P.
30-JUN-2000; 2000US-0215688P.
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                                    31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schneider P, Thompson J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antagonist.
AAE00506;
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infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia,

inhibiting the proliferation of tumour cells. (I) is useful for

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designated Ztnfr12 (1). (1) has cytostatic, immunosuppressive, dermatological, antiinflammatory, neuroprotective, antidiabetic, antirheumatic, antiarthmatic, nephrotropic and hypotensive activities, and can be used in gene therapy. (1) can be used for inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12 (e.g. ZTNF4), for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
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diseases, renal disorders, B-cell lympho-proliferative disorders, immunosuppressive diseases, organ transplantation, inflammation and human immunodeficiency virus (HIV), and for treating, suppressing or altering an immunote response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. The present sequence is human APRIL-R also referred as BCMA or BCM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated human tumor necrosis factor receptor polypeptide, termed Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease.
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive, dermatological; antinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritic; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
                                                                                                                                                                                                                                                                                           MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                1 MLOMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                    Length 184;
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                                                                                                                                                                                    100.0%; Score 51; DB 4; I 100.0%; Pred. No. 4.1e-47;
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                                                                                                                                                                                                                       0; Mismatches
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20-DEC-2000; 2000US-0257131P.
28-JUN-2001; 2001US-0302715P.
29-AUG-2001; 2001US-0315565P.
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                                                                                                                                                                                                   Local Similarity 100.
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                                                                                                                                                 Sequence 184 AA;
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Matches
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          Infinituring the principal system of the properties of the production and cytokine production and for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. The present sequence represents a protein which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genes that are up- or down-regulated in colorectal cancer, useful for diagnosing colorectal cancer in a subject, or for identifying modulators of colorectal cancer-associated proteins and genes for treating
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; metastasis; differential expression; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                                                 100.0%; Score 51; DB 5; Length 184; 100.0%; Pred. No. 4.1e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; gene therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                            51; Conservative
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                Sequence 184 AA;
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Sequence 184 AA;
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                                                                                                                                                                          AAE35216;
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                                            Best Loc
Matches
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                                                                ö
                                                                                                                                                                                                                                                Human; tumour; B-cell maturation antigen; transmembrane activator; calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy; neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease; non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma; BCMA; multiple myeloma.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B-cell maturation antigen and transmembrane activator and calcium-modulator and cyclophilin ligand-interactor, useful for treating disorders e.g. inflammation or lymphoma.
                                                                                      51
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                                                                                      1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG
                                           Length 184;
                                                                Indels
                                           100.0%; Score 51; DB 5; I 100.0%; Pred. No. 4.1e-47; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                     "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                'note= "Antigenic epitope"
                                                                                                                                                                                                                                 Human B-cell maturation antigen (BCMA).
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                                                                                                                                                                  AAE28961 standard; protein; 184 AA.
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12-APR-2001; 2001US-0283447P.
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                                                                                                                                                                                                            (first entry)
                                                                  51; Conservative
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                                                     Local Similarity
 therapeutic value
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                       Sequence 184 AA;
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                                             Query Match
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephrius; acthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; B-cell maturation receptor; BCMA; receptor.
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                                                                                                   Gaps
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                                                                                                                                                                        27
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Best Local Similarity 100.0%; Pred. No. 4.1e-47;
Matches 51; Conservative 0; Mismatches 0; Indels
                                 Length 184;
                                                                                                   Indels
                             Score 51; DB 5; 1
Pred. No. 4.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human B-cell maturation receptor (BCMA) protein.
100.0%; Scc...
100.0%; Pred. No....
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAE35216 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAY-2002; 2002WO-US015910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-2001; 2001US-0293343P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rixon MW, Gross JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-148455/14.
                                                                  Local Similarity
Les 51; Conserv
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Best Local Similarity

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The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID No.2, or amino acids 134-285 of SEQ ID NO.2, by at least one modification in the region connecting &bgr; strands D and B that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antitheumatic, antidiabetic, neuroprotective, antiathyroid, antipyretic, nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 a vaccine. A protein of the invention is useful for inhibiting TALL-1 of the strands autoimmune diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis, chrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, chrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis and caute rheumatic fever, post-streptococcal glomerulonephritis and constructions the present sequence represents human BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
                                                                                                                                                                                                                                                                                                                human; TALL-1; antagonist; immunosuppressive; antirheumatic; antinflammatory; antiarthritic; dermatological; antidiabetic; neuroprotective; antithyrotd; antipyretic; nephrotropic; vasotropic; vaccine; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple solerosis; myasthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura; goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.
                        1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51
1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NAJE-) NAT JEWISH MEDICAL & RES CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 62; Page 613; 618pp; English.
                                                                                                                                                 ADA49361 standard; protein; 184 AA.
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14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
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                                                                                                                                                                                                                                    20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shu H, Liu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-403345/38.
N-PSDB; ADA49360.
                                                                                                                                                                                                                                                                              Human BCMA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003035846-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                       RESULT 12
                                                                                                                               ADA49361
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100.0%; Score 51; DB 6; Length 184;

Query Match

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The invention relates to a novel antibody or its fragment, which

The invention relates to a novel antibody or its fragment, which

The antibody of the invention has dermaclogical, immunosuppressive,

antiallargic, antiathemmic, antibarthritic, cytostatic, antianaemic,

antiallargic, antiathmatic, neuroprotective, ophthalmological,

tubercollostatic, antidabetic, antipsoritatic, and halogical,

antiarteriosclerotic, vasotropic, thyromimetic, and halogical,

the antibody or its fragment are useful for treating, preventing or

ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in

host disease or disorder such as autoimmune disease, and graft versus

complexed the autoimmune disease is systemic lupus

crythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody

crythematosus, rheumatoid arthritis or Sjogren's syndrome and inflammatory

crythematosus actecting, diagnosing, prognosing, treating, preventing or

ameliorating a disease or disorders associated with aberrant APRIL or

APRIL receptor expression or aberrant function of APRIL or APRIL

creeptor. The disease or disorders includes autoimmune and inflammatory

disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,

asthma, allergic encephalowyelitis, myocarditis, multiple sclerosis,

uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune

creating, practicularly B cell cancers, immunodeficiency syndrome, Bruton's disease

crystem, particularly B cell cancers, immunodeficiency syndrome (AIDS)), and

creatious diseases (e.g. acquired immunodeficiency syndrome represents

proliferative disorders (e.g. leukemia). The present sequence represents
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                APRIL; scFV; immunospecific; tumour necrosis factor delta; TNF-delta; dermatological; immunosuppressive; antiinflammatory; antirheumatic; antiartitic; cyfostatic; antianemic; antiallergic; antiastheumatic; antiproprotective; ophthamological; tuberculostatic; antidiabetic; antiproprotectic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; antidamence; autoimmune disease; graft versus host disease; GVHD inflammatory disorder; proliferative disorder; single chain antibody; antibody; human; BCMA; tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Non-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
                                     Gaps
                                                                             1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                         ö
                                   Indels
                Pred. No. 4.1e-47;
Mismatches 0;
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                                                                                                                                                                                                                                            ABP60552 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                             Human tumour necrosis factor BCMA.
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-2002; 2002WO-US016106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-2001; 2001US-0293100P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                     51; Conservative
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                                                                                                                                                                                                                                                                                         ABP60552;
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ABP60552
                                       Matches
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Matches

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The present invention describes an isolated polymucleotide (I), which is overexpressed in haematological malignancies, and which encodes a coverexpressed in haematological malignancies, and which encodes a polypeptide or an immunogenic fragment of the polypeptide. Also described: (1) an isolated polypeptide; (2) an expression vector comprising (I) operably linked to an expression control sequence; (3) a host cell comprising an expression vector; (4) an isolated antibody that specifically binds to the polypeptide or its immunogenic fragment; and (5) immunoconjugates comprising the antibody above, or an antibody that specifically binds to a polypeptide, or its immunogenic fragment, encoded by (I). (I) has cytostatic and immunotherapy. The immunoconjugates are useful in the manufacture of a medicament, particularly as active ingredients in a composition for treating canner, e.g. multiple myelome cell, chronic leukaemia, B cell leukaemia, B unltiple myelomes in humans, sheep, primates, goats, bovines, equines, porcines, lupines, canines or felines. The polymucleotide (I) or polypeptide can be used for screening anti-cancer agents, and generating antibodies or immunoconjugates for treating or preventing the above-mentioned diseases. The polymucleotide, the manufacture of an altibody can be used for detecting, diagnosing or polymentic or antibody can be used for detecting, diagnosing or properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prognosticating the haematological malignancies described above. The present sequence is used in the exemplification of the present invention.
                                                                              haematological malignancy; immunoconjugate; cytostatic; immunostimulant; vaccine; immunotherapy; cancer; multiple myeloma cell; chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hematological malignancy-related genes and polypeptides, useful for screening anti-cancer agents, and generating antibodies or immunoconjugates for treating e.g. multiple myeloma cell or chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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Pred. No. 4.1e-47;
Mismatches 0;
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Pred. No. '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2, 2006, 04:23:29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; SEQ ID NO 4; 307pp; English.
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100.0%; Pred
                                       Human Ly1732P protein SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                   22-JAN-2003; 2003WO-US002353.
                                                                                                                                                                                                                                                                                                                                                          22-JAN-2002; 2002US-00057475
15-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Algate PA,
Mcneill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphocytic leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-598749/56.
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Job time : 187 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 184 AA;
                                                                                                                                                                                                                                  WO2003062401-A2.
                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                            31-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carter L,
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                                                                                                                                                  human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a human BCMA polypeptide. The specification also describes TACI and BR3 polypeptides. TACI and BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April bind to the TACI receptor, while TMF family ligands TALL-1 also binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for preparing a composition for treating systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, TACI, BR3; receptor, tumour necrosis factor ligand; TNF ligand;
TALL-1; April; systemic lupus erythematosus; BCMA.
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                                                                                                                              Gaps
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                                                                                  100.0%; Score 51; DB 6;
100.0%; Pred. No. 4.1e-47
iive 0; Mismatches 0
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100.0%; Pred. No. 4.1e-47
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid seguence of human BCMA receptor.
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                                                                                                                                                                                                                                                                                                                     ABP97717 standard; protein; 184 AA
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  the tumour necrosis factor BCMA
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30-APR-2002; 2002US-0377171P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-2002; 2002WO-US023487
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                        Local Similarity 100.
nes 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-256560/25.
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                                           Sequence 184 AA;
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                                                                                                                                                                                                                                                                                                                                                            ABP97717;
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Length 184; Indels 21 51

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RESULT 15

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Best Loca Matches

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

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US-10-077-438-1\_COPY\_1\_51 51 1 MLQMAGQCSQNEYFDSLLHA......TPPLTCQRYCNASVTNSVKG 51 Title: Perfect score:

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283416 segs, 96216763 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

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1: pirl:\*
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3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		dŧ			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	51	100.0	184	7	S43486	B-cell maturation
71	7	13.7	309	N	E72365	conserved hypothet
e	7	13.7	5188		B85547	probable RTX famil
4	7	13.7	5291	~	F90696	hypothetical prote
ß	9	11.8	113	~	B72242	
9	9	11.8	129	N	A81187	2.
7	9	11.8	148	~	B58345	myoglobin - tremet
80	9	11.8	223	7	S16652	hypothetical prote
<b>,</b>	9	11.8	237	7	T24407	hypothetical prote
10	9	11.8	240	7	A96697	protein F1N21.18 [
11	9	11.8	245	~	T36127	ble ribonu
12	9	11.8	249	ä	T45217	rec7 protein - fis
13	9	11.8		7	E89124	ij
14	ý	11.8	269	7	AC0404	probable deoR-fami
15	9	11.8	283	~	C86535 ·	hypothetical prote
16	9	11.8	283	~	H72087	hypothetical prote
17	9	11.8	303	~	T17774	
18	9	11.8	311	~	C69464	н
19	φ	11.8	321	-	QQEC15	hypothetical 34K p
20	9	11.8	321	~	F91104	hypothetical prote
21	9	11.8	321	7	A85950	hypothetical prote
22	9	11.8	327	7	361660	probable membrane
23	9	11.8	338	7	A82209	conserved hypothet
24	9	11.8		7	T41126	meiotic recombinat
25	9	11.8		~	B96632	hypothetical prote
26	9	٠		~	H75446	(S) -2-hydroxy-acid
27	9	11.8		-	OKBYC3	
28	9	11.8	404	7	S64944	
29	9	11.8	460	~	H69095	carbon monoxide de

conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Il-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004
C;Accession: E72365
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

RESULT 2 E72365

hypothetical prote hypothetical prote		triacylglycerol li CTP synthase (BC 6 hymothetical prote	œ · · · ·	hypothetical prote rpfC protein - Xan hypothetical prote .hypothetical prote
T30794 T28480	A/ZISS E42508 D36841	A28997 T01513	C69161 S62567 D96775	T11641 S16003 T29204 G95094
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11.8				11.8
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30	2 E E C	3 9 6 c	2 6 4 4 2 6 0 4	4 4 4 4 C1 E2 4 72

## ALIGNMENTS

	RESULT 1
	5-43-40 B-cell maturation factor - human
	N,Alternate names: BCM protein; BCMA protein; BEL protein
	C;Species: Homo sapiens (man)
	C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
	C; Accession: S43486; S31208; S36661
	R, Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, K.; Larsen, C.J.; Isapis, A.
	Nucleic Acids Res. 22, 1147-1154, 1994
	Ajilles ine Burk gene, pieterentaliy expressed during b fympholu macuraci, is mere b peference number: 643486: MITD:9421875: PMID:8165126
	A. Accession: 843486
	A;Status: preliminary
	A; Molecule type: DNA
	A/Residues: 1-184 <laa></laa>
	A;Cross-references: UNIPROT: 002223; UNIPARC: UP10000034D1B; EMBL: 2295/4; NID: 94 / 1244; P.1
	Ribaabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, K.; Larben, C.U.; Isapis,
	EMBO J. 11, 3897-3904, 1992
	Affile: A new gene, BCM, on Chromosome is as tused to the interleukin 2 gene by a clay
	A; Reference inducer: 531208; MulD:9301098; FMID:1330303
	A ACCESSION STATE
	A MOLECULE LYPE HINNA A POLICULE LYPE HINNA
	A REBIGUES: ILT. CAA78679.1: PI
	A. Arresagion - Staff of 1
	Association of the second of t
	A. Wolecule type: mRNA
	ArResidues: 4-184 <la3></la3>
	A:Cross-references: UNIPARC:UPI0000046868; EMBL:Z14955
	C;Genetics:
	A; Gene: GDB: BCMA
	A;Cross-references: GDB:135977; OMIM:109545
	A;Map position: 16p13.1-16p13.1
	A;Introns: 44/1; 93/1 -
	C;Superfamily: human B-cell maturation factor
	3 2; Length 184; ie-47;
	Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	Qy 1 MLQMAGQCSQNBYFDSLLHACIPCQLRCSSNTPPLJCQRYCNASVTNSVKG 51
,	Db 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNIPPLITCQRXCNASVINSVKG 51.

Gaps

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Indels

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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72224
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9X1M0; UNIPARC:UPI00000C126C; GB:AE001800; GB:AE000512; NID!
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type IV pilin protein NWB0547 [imported] - Neisseria meningitidis (strain MC58 serogroup) c; Species: Neisseria meningitidis C; Date: 31 Mar-2000 #text_change 09-Jul-2004 C; Date: 31 Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C; Date: 31 Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 R; Tettelin, H; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherry, B.A.; i, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 A; Muthors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; A; Reference number: A81000; MUID:20178755; PMID:10710307
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A;Cross-references: UNIPROT:Q9KON9; UNIPARC:UPI00000C44EE; GB:AE002410; GB:AE002098; NIE
A;Experimental source: serogroup B, strain MC58
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C;Superfamily: Thermotoga maritima hypothetical protein TM1534
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Best Local Similarity 100.0%; Pred. No. 73; Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 35;
Live 0; Mismatches
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                                                                                             43 ASVTNSV 49
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-113 <ARN>
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                                                            Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A;Ritle: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A;Reference number: A72200; MUD:99287316; PMID:10360571

A;Accession: E72365

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-309 <ARN>

A;Residues: 1-309 <ARN>

A;Crosse-references: UNIPROT:Q9WYY9; UNIPARC:UPI00000C13FC; GB:AE001728; GB:AE000512; NIE
C;Genetics:
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R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A, Reference number: A99629; MUID:21156231; PMID:11258796
A, Status: Prediminary
A, Molecule type: DNA
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A;Cross-references: UNIPROT:Q8X2T1; UNIPARC:UPI000011021F; GB:BA000007; PIDN:BAB33965.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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      Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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100.0%; Pred. No. 6.2
tive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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A;Residues: 1-148 <RAS.
A;Cross-references: UNIPROT:P80722; UNIPARC:UPI000012B54D
A;Note: monomeric myoglobin with a tyrosine at posistion B10 and B7(distal position) res
C;Superfamily: trematode myoglobin; globin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Microbiol. 5, 1863-1872, 1991
A;Title: Structure of two retrons of Escherichia coli and their common chromosomal inser
A;Reference number: S16652; MUID:92114764; PMID:1722556
A;Accession: S16652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-237 <WIL>
A;Cross-references: UNIPROT:Q22118; UNIPARC:UPI00000827F9; EMBL:Z74041; PIDN:CAA98521.1;
A;Experimental source: clone T03F7
                                                          R,Rashid, A.R.; Van Hauwaert, M.; Haque, M.; Siddiqi, A.H.; Lasters, I.; De Mayer, M.; submitted to the Protein Sequence Database, October 1996
A,Description: Trematode myoglobins: functional molecules with a distal tyrosine.
A,Reference number: A58345
A,Accession: B58345
A,Status: preliminary
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C;Species: Bscherichia coli retron Ec86
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Jul-1998
C;Accession: S16652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24407
R;Mortimore, B.
                      Date: 23-May-1997 #sequence_revision 23-May-1997 #text_change 12-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                              11.8%; Score 6; DB 2; Length 148; 100.0%; Pred. No. 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T03F7.6 - Caenorhabditis elegans
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A;Accession: T24407
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.8%; Score 6; DB 2;
100.0%; Pred. No. 56;
vative 0; Mismatches
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Matches 6; Conservative 0; Mismatches
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A;Introns: 12/1; 53/1; 117/3; 168/3; 191/3
Species: Isoparorchis hypselobagri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain B
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Best Local Similarity
Matches 6; Conserval
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-223 <LIM>
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                                               Accession: B58345
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protein FIN21.18 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Spacession: A96697) (Spacession: A96697) (Spacession: A96697) (Spacession: A96697) (Spacession: A96697) (Spacession: Apacession: A
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A;Cross-references: UNIPROT:Q9S2H7; UNIPARC:UPI0000134469; EMBL:AL096852; PIDN:CABS0985
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R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
AjAccession: T36127
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C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Schizosaccharomyces pombe
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100.0%; Pred. No. 60;
:ive 0; Mismatches
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100.0%; Pred. No. 61;
ive 0; Mismatches
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Matches 6; Conservative
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Search completed: March 2, 2006, 04:28:14 Job time : 40 secs
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Protein K07C11.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89124
C;Accession: E89124
C;Accession: E89124
C;Accession: E89124
C;Accession: E89124
C;Accession: E89124
A;Title: Genome sequence of the nematode C elegans: a platform for investigating biolog
A;Title: Genome sequence of the nematode C elegans: a platform for investigating biolog
A;Nete: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Scatus: preliminary
A;Wolecule type: DNA
A;Residues: 1-257 <STO>
A;Coss-references: UNIPROT:Q21272; UNIPARC:UPI0000077A84; GB:chr_V; PIDN:AAA96181.1; PI
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A; Preference number: AB0001; MUID:21470413; PMID:11586360
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A; Status: preliminary
A; Molecule type: DNA
A; Medlecule s: 1-269 < KUR>
A; Cross-references: UNIPROT: Q8ZBS6; UNIPARC: UPI0000DC895; GB: AL590842; PIDN: CAC92559.1;
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100.0%; Pred. No. 62;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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C;Accession: C86535
KiShirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-283 <STO>
A;Cross-references: UNIPROT:Q9Z816; UNIPARC:UPI0000047124; GB:BA000008; NID:g8978729; PI
A;Experimental source: strain J138
C;Genetics:
                                                                                                                                                                                                                                                                                                    hypothetical protein CPj0357 [imported] - Chlamydophila pneumoniae (strain J138)
C,Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                            Length 269;
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                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.8%; Score 6; DB 2;
100.0%; Pred. No. 69;
tive 0; Mismatches
                                                                          DB 2;
                                                                                                                   0; Mismatches
              A,Gene: YPO3327
C,Superfamily: fuc operon regulatory protein
                                                                            Score 6; I
Pred. No.
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100.0%; Fig.
                                                                          11.8%;
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                                                                                                                   Conservative
                                                                                                                                                                                                    136 VTNSVK 141
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                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                              45 VTNSVK 50
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C, Genetics:
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Sequence

Sequence Sequence Sequence Sequence

Sequence

Sequence 17, Appl Sequence 10, Appl Sequence 10, Appl Sequence 263362, Sequence 221552, Sequence 342318, Sequence 34218, A

Sequence Sequence

Title: Perfect score:

Run on:

Sequence:

Searched:

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1 MLQMAGQCSQNEYFDSLLHACIPCQRCSSNTPPLTCQRYCNASVTNSVKG. 51
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100.0%; Score 51; DB 4; Length 18
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels
US-10-077-137-3
US-09-854-864-7
US-09-854-864-13
US-09-855-158-13
US-10-145-206-197
US-09-855-158-12
US-09-855-158-12
US-09-854-18-11
US-09-855-158-11
US-10-216-074-17
US-09-854-864-10
US-10-216-074-17
US-09-854-864-10
US-09-855-115-263362
US-10-425-115-263362
US-10-425-115-342318
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US-10-425-114-342318
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APPLICANT: Barowning, Jeffrey
APPLICANT: Technope, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Schneider, Pascal
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCWA), An
TITLE OF INVENTION: 1000-CC-18
FILE REFERENCE: A0800-CT-18
FILE PRIOR PLILING DATE: 2000-02-18
FRIOR FILING DATE: 2000-02-11
FRIOR FILING DATE: 2000-02-118
FRIOR FILING DATE: 2000-02-118
FRIOR PRILING DATE: 2000-02-118
FRIOR PRILING DATE: 2000-02-18
FRIOR PRILING DATE: 2000-02-18
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10077438; Publication No. US20020165156A1; GENERAL INFORMATION: APPLICANT: MacKay, Fabienne
      ORGANISM: homo sapien
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LENGTH: 184
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Sequence 2, A
Sequence 47,
Sequence 8, A
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51
1 MLQMAGQCSQNEYFDSLLHA.....TPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                            March 2, 2006, 04:38:58 ; Search time 164 Seconds
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1. /cgn2 6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2. /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3. /cgn2 6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
4: /cgn2 6/ptodata/1/pubpaa/USOAP.puBCOMB.pep:*
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6: /cgn2 6/ptodata/1/pubpaa/USII_PUBCOMB.pep:*
                                         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-068-125-2

US-10-115-192-8

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US-10-123-363A-27

US-10-182-363A-27

US-10-182-363A-27

US-10-182-363A-27

US-10-142-634-9

US-10-626-914-6

US-10-626-914-6

US-10-989-826-46

US-10-989-826-46

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US-10-989-826-46

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US-10-115-192-12

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US-09-855-158-6

US-09-855-158-6
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100.0%; Score 51; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels
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Publication No. US2020172674A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MacKay, Fabienne
APPLICANT: Ambrose, Christine
APPLICANT: Tschopp, Jurg
APPLICANT: Tschopp, Jurg
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Appced, Inc.
APPLICANT: Apporen, Inc.
APPLICANT: Applicant Applic
                                                                       APPLICANT: INCURPOSAL, CELLLY
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT APPLICATION NUMBER: US/10/077,438
FRIOR FILING DATE: 2002-02-18
FRIOR FILING DATE: 1999-08-17
FRIOR FILING DATE: 2000-02-11
FRIOR APPLICATION NUMBER: 60/181,684
FRIOR FILING DATE: 2000-02-18
Schneider, Pascal
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                                                           Thompson,
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
FILE OF INVENTION: Antibodies That Bind Both BCMA and TACI
CURRENT APPLICATION NUMBER: US/10/068,725
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/270,74
PRIOR APPLICATION NUMBER: 60/283,447
PRIOR FILING DATE: 2001-04-12
RIOR FILING DATE: 2001-04-12
SCOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 100.0%; Score 51; DB 4; I Similarity 100.0%; Pred. No. 3.1e-45; 51; Conservative 0; Mismatches 0;
                                                                                   GENERAL INFORMATION:
GREEKAL INFORMATION:
APPLICANT: AUGROSE, Christine
APPLICANT: AUGROSE, Christine
APPLICANT: Techopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Immunoregulatory Agent
FILE REPERENCE: A080PCT
TITLE OF INVENTION: Immunoregulatory Agent
FILE REPERENCE: A080PCT
CURRENT APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/10068725; Publication No. US20030012783A1; GENERAL INFORMATION:
Sequence 7, Application US/10077137 Publication No. US20020172674A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
Matches 51; Conserv
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RESULT 6

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CURRENT APPLICATION NUMBER: US/10/008,063
                    2001-11-05
                                                                                                                       TYPE: PRT , ORGANISM: Homo sapiens US-10-008-063-7
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US-10-152-363A-27
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ORGANISM: Homo sapiens
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US-10-152-363A-27
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LENGTH: 184
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                                                                                       APPLICANT: Ruben, Steven M.
TITLE OF INVENTIVES.
FILE REPRENCE: PF554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT APPLICATION NUMBER: US/10/151,882
PRIOR APPLICATION STEEN SONZ-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR PILING DATE: 2001-05-24
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APPLICANT: Biogen, Inc.
TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
FILE REFERENCE: A083PCT
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CURRENT FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 60/215688
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/181807
PRIOR APPLICATION NUMBER: 60/157933
PRIOR APPLICATION NUMBER: 60/157933
PRIOR PILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PASTSEQ for Windows Version 4.0
                    Sequence 47, Application US/10151882
Publication No. US20030059862A1
GENERAL INFORMATION:
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Publication No. US20030082175A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 51; Conservative 0
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
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APPLICANT: Xu, Wenfeng
APPLICANT: Henne, Randal M.
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Best Local Similarity 100.
Matches 51; Conservative
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US-10-151-882-47
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                                                                                                                                                                                                                                                                                    SEQ ID NO 47
LENGTH: 184
TYPE: PRT
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Sequence 11, Application US/10216074
Sequence 11, Application No. US20030148445A1
GENERAL INFORMATION:
APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/10/216,074
CURRENT FILING DATE: 2003-03-12
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                                                                                                                                                                                                     Score 51; DB 4; Length 184;
Pred. No. 3.1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rixon, Mark W.
APPLICANT: Gross, Jane A.
IITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REFERENCE: 01-20
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100.0%; Pred. No. c.
0; Mismatches
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NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/293,343
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: US/09/565,423
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PRIOR APPLICATION NUMBER: 60/132,892
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/10152363A Publication No. US20030103986A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: UNKNOWN
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Best Local Similarity 100.1
Matches 51; Conservative
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; Sequence 6, Application US/10485489
; Publication No. US20050070689A1
; GENERAL INFORMATION:
    APPLICAMT: Dixit, Vishva
; APPLICAMT: Grewal, Iqbal
; APPLICAMT: Ridgway, John
; TITLE OF INVENTION: TACIB and BR3 Polypeptides and Uses Thereof
; FILE REFERENCE: IL669.1750SWO
; CURRENT APPLICATION NUMBER: US/10/485,489
; CURRENT PILING DATE: 2004-01-30
; PRIOR PILING DATE: 2002-07-24
; PRIOR PILING DATE: 2001-08-03
; PRIOR PILING DATE: 2001-08-03
; PRIOR PILING DATE: 2001-08-03
; PRIOR FILING DATE: 2001-08-03
; PRIOR FILING DATE: 2001-08-03
; RIOR PILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                      1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                           Length 184;
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Sequence 6, Application US/10626914

Publication No. US20050043516A1

GENERAL INFORMATION:
Patin Docket Preview

APPLICANT: CHUNTHARAPAI, ANAN

APPLICANT: GREWALL, IQBAL

APPLICANT: YAN, MINHONG

TITLE OF INVENTION: TACI Antibodies and Uses Thereof
FILE REFERENCE: P1942R1

CURRENT APPLICATION NUMBER: US/10/626,914

CURRENT FILING DATE: 2003-07-25

FRIOR FILING DATE: 2002-07-25

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 6
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100.0%; Pred. No. 3.1e-45;
tive 0; Mismatches 0;
                                                                                      ch 100.0%; Score 51; DB 4; I Similarity 100.0%; Pred. No. 3.1e-45; 51; Conservative 0; Mismatches 0;
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Best Local Similarity 100..
Best 51; Conservative
                    ; ORGANISM: Homo sapiens
US-10-742-634-9
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                                                                                                               Best Local Similarity
Matches 51; Conserv
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Best Local Similarity
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                                                                                           Query Match
TYPE: PRT
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Sequence 39, Application US/10087080

Publication No. US2003023820A1

GENERAL INFORMATION:

APPLICANT: Markowitz, Sanford David

APPLICANT: Markowitz, Sanford David

APPLICANT: Case Western Reserve University

TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for

TITLE OF INVENTION: Modulators of Metastatic Colorect

TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer

TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer

TITLE OF INVENTION WUMBER: US/10/087,080

CURRENT FILING DATE: 2001-02-27

PRIOR PILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: US 60/281,149

PRIOR FILING DATE: 2001-04-02

PRIOR FILING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 39

LENGTH: 184
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Sequence 9, Application US/10742634
Publication No. US20040208824A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fall Halbert, David
APPLICANT: Hilbert, David
APPLICANT: Hilbert, David
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses THILE OF INVENTION: NUMBER: US/10/742,634
CURRENT APPLICATION NUMBER: US/10/742,634
CURRENT FILING DATE: 2003-12-22
PRIOR FILING DATE: 2002-12-22
PRIOR FILING DATE: 2003-12-22
PRIOR FILING DATE: 2003-12-22
PRIOR FILING DATE: 2003-12-22
PRIOR FILING DATE: 2003-05-02
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                                                                      Gaps
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OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
OTHER INFORMATION: 17 (TNFRSF17)
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                                                                                                                       1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVINSVKG 51
                                                                                                                                                          1 MLQMAGQCSQNBYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                      Length 184;
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                      100.0%; Score 51; DB 4; Length 18
100.0%; Pred. No. 3.1e-45;
ive 0; Mismatches 0; Indels
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100.0%; Score 51; DB 4; I
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0;
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SEQ ID NO 9
LENGTH: 184
       Query Match
Best Local Similarity 100.0°
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                RESULT 11
US-10-087-080-39
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                                                   1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                           RESULT 15
US-10-861-049-27
| Sequence 2.7, Application US/10861049
| Publication No. US2050095243A1
| GENERAL INFORMATION:
| APPLICANT: Andrew Chan
| APPLICANT: Andrew Chan
| APPLICANT: Glad Gong
| APPLICANT: Glad Gong
| TILE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
| TILE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
| TILE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
| TILE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
| TILE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
| TILE OF PARTIES 2003-06-06
| PRIOR PILING DATE: 2003-06-06
| PRIOR PILING DATE: 2003-06-05
| SEQ ID NO 27
| LENGTH: 184
| TYPE: PRI
| TYPE: PRI
| CRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 3.1e-45;
Matches 51; Conservative 0; Mismatches 0; Indels
0; Indels
  0; Mismatches
     51; Conservative
     Matches
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Search completed: March 2, 2006, 04:42:13 Job time : 165 secs

1 MLQMAGQCSQNBYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51

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                                                                                                                 March 2, 2006, 04:39:33 ; Search time 21 Seconds
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Perfect score:
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# 135339 Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

/pubpaa/PCT NEW FUB.pep /pubpaa/US09 NEW PUB.pep /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB. Published April 1: /cgn2\_6/)
2: /cgn2\_6/)
3: /cgn2\_6/) cgn2\_ Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length	DB	ΩI	Description
-	51	100.0	184	9	US-10-742-634-9	Sequence 9, Appli
7	51	100.0	184	9	US-10-967-527A-8	φ,
m	51	100.0	184	7	US-11-242-294-27	27,
4	40	78.4	40	9	US-10-967-527A-9	Sequence 9, Appli
S	10	19.6	185	ω.	US-10-967-527A-10	Sequence 10, Appl
9	7	13.7	5291	7	US-11-052-554A-281	Sequence 281, App
ć	Ġ	11.8	231	7	US-11-100-183-37	Sequence 37, Appl
ĕ	ø	11.8	313	,	US-11-098-686-10357	
6	9	11.8	379	7	US-11-072-512-3298	٠,
10	9	11.8	398	7	US-11-132-142-7	Sequence 7, Appli
11	9	11.8	572	7	US-11-072-512-3907	٠,
12	9	11.8	605	ø	US-10-689-742-140	Sequence 140, App
13	9	11.8	668	7	US-11-087-099-5101	
14	9	11.8	166	9	US-10-821-234-1691	1691,
15	9	11.8	800	7	US-11-072-512-3534	3534
16	9	11.8	1137	7	US-11-012-762-70	
17	φ	11.8	1461	7	US-11-052-554A-283	Sequence 283, App
18		11.8	5405	7	US-11-108-172-1116	1116,
19	Ŋ	8.6	60	7	US-11-045-024-496	•
20	'n	9.8	80	7	US-11-045-024-1697	
21	'n	9.8	80	7	US-11-045-024-1698	Sequence 1698, Ap
22	Ω.	9.8	80	7	US-11-045-024-3636	Sequence 3636, Ap
23	Ŋ	9.8	80	7	US-11-045-024-4379	Sequence 4379, Ap
24	Ŋ	9.6	œ	7	US-11-045-024-4380	Sequence 4380, Ap
25	Ŋ	9.8	00	7	US-11-045-024-6787	Sequence 6787, Ap

Sequence 6953, Ap	Sequence 7898, Ap	Sequence 12102, A	Sequence 12785, A	Sequence 265, App	Sequence 643, App	Sequence 644, App	Sequence 3241, Ap	Sequence 4503, Ap	Seguence 6790, Ap	Sequence 6958, Ap	Sequence 10213, A	Sequence 12084, A	Sequence 13797, A	Sequence 13801, A	Sequence 13803, A	Sequence 713, App	Sequence 736, App	Sequence 30, Appl	Sequence 303, App	
US-11-045-024-6953	US-11-045-024-7898	US-11-045-024-12102	US-11-045-024-12785	US-11-045-024-265	US-11-045-024-643	US-11-045-024-644	US-11-045-024-3241	US-11-045-024-4503	US-11-045-024-6790	US-11-045-024-6958	US-11-045-024-10213	US-11-045-024-12084	US-11-045-024-13797	US-11-045-024-13801	US-11-045-024-13803	US-11-136-079-713	US-11-136-079-736	US-11-152-747-30	US-11-045-024-303	
7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	
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56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses T
FILE REFERENCE: 1488.1810002.
CURRENT PELLORITON UNMBER: US/10/742,634
CURRENT FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: US 60/435,262
PRIOR APPLICATION NUMBER: US 60/467,198
PRIOR PILING DATE: 2003-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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APPLICANT: Fox, Brian A.
APPLICANT: Holloway, James L.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Zenfri4, A Tumor Necrosis Factor
TITLE OF INVENTION: Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 51; DB 6; 1
100.0%; Pred. No. 8.3e-48;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/967,527A CURRENT FILING DATE: 2004-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/10967527A Publication No. US20050256041A1
Sequence 9, Application US/10742634 Publication No. US20050249671A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
                                                                 APPLICANT: Parmelee, David
APPLICANT: Yeh, Ren-Hwa
APPLICANT: Galperina, Olga
APPLICANT: Hilbert, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 03-17
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LENGTH: 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-LIL-42-22-27, Application US/11242294

| Publication No. US20060034852A1
| GENERAL INFORMATION:
| APPLICANT: Rixon, Mark W. |
| APPLICANT: Gross, Jane A. |
| TILLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins FILE REFREENCE: 01-20
| FILE REFREENCE: 01-20
| FILE REFREENCE: 01-20
| FRICH FILING DATE: 2005-10-03
| PRIOR FILING DATE: 2005-10-03
| PRIOR PILING DATE: 2001-05-20
| FRIOR FILING DATE: 2001-05-24
| NUMBER OF SEQ ID NOS: 70
| SOFTWARE: FastSEQ for Windows Version 3.0
| SEQ ID NO 27
| LENGTH: 184
                                                                                                                                                                                                                                                                  0; Indels
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Publication No. US20050256041A1
GENUREAL INFORMATION:
APPLICANT: Fox, Brian A.;
APPLICANT: Sheppard, Paul O.;
TITLE OF INVENTION: Enfirl4, A Tumor Necrosis Factor;
TITLE OF INVENTION: Enfirl4, A Tumor Necrosis Factor;
TITLE OF INVENTION: Enceptor;
CURRENT APPLICATION NUMBER: US/10/967,527A;
CURRENT FILING DATE: 2004-10-18
PRIOR APPLICATION NUMBER: 60/511,698
MINDER FILING DATE: 2003-10-16
                                                                                                                                                                                                                     Query Match
100.0%; Score 51; DB 6; I
Best Local Similarity 100.0%; Pred. No. 8.3e-48;
Matches 51; Conservative 0; Mismatches 0;
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Pred. No. 8.3e-48;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 40
TYPE: PRT
ORGANISM: homo sapiens
FEATURE:
PRIOR APPLICATION NUMBER: 60/511,698
PRIOR FILING DATE: 2003-10-16
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 184
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Best Local Similarity 100.0%;
Matches 51; Conservative 0
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CRGANISM: Homo sapiens
US-11-242-294-27
                                                                                                                                    TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-11-242-294-27
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US-11-052-554A-281
Sequence 281, Application US/11052554A
Publication No. US2005028866A1
PublicANT: Sachdeva, et al.
PITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
PITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
PITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
PITLIANT PRILIANT DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR PILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-02-06
PRIOR FILING DATE: 2004-02-06
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                                                                                                                                                                0; Indels
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Sequence 10, Application US/10967527A

Publication No. US20050256041A1

Publication No. US20050256041A1

GENERAL INFORMATION:

APPLICANT: Fox, Brian A.

APPLICANT: Holloway, James L.

APPLICANT: Holloway, James L.

TITLE OF INVENTION: Zenff14, A Tumor Necrosis Factor

TITLE OF INVENTION: Zenff14, A Tumor Necrosis Factor

TITLE OF INVENTION: Receptor

FILE REPRENCE: 03-17

CURRENT APPLICATION NUMBER: 06/511,698

PRIOR APPLICATION NUMBER: 60/511,698

PRIOR APPLICATION NUMBER: 60/511,698

PRIOR APPLICATION NUMBER: 60/511,698

NUMBER OF SEQ ID NOS: 51

SOSTWARE: FRASEZQ for Mindows Version 4.0
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                                                                                                                                                                                                                                                 1 GQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                                                                                                                                                                                   6 GQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                                                                           Query Match 78.4%; Score 40; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 1.5e-36;
Matches 40; Conservative 0; Mismatches 0;
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13.7%; Score 7; DB 5
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches
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US-11-052-554A-281
, LUCATION: (1)...(40); OTHER INFORMATION: cysteine rich US-10-967-527A-9
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SOFTWARE: Patentin version 3.3
SEQ ID NO 281
LENGTH: 5291
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Best Local Similarity 100.
Matches 10; Conservative
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LENGTH: 185
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APPLICANT: The Burnham Institute
APPLICANT: Sikora, Sergey
APPLICANT: Sikora, Sergey
APPLICANT: Sikora, Sergey
APPLICANT: Godaik, Adam
TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
FILE REFERENCE: 8014-011-US
CURRENT APPLICATION NUMBER: US/11/132,142
CURRENT FILING DATE: 2005-05-17
PRIOR PLING DATE: 2004-05-17
PRIOR FILING DATE: 2004-05-17
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11.8%; Score 6; DB 7,
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches
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Mismatches
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PRIOR PELICATION NUMBER: US 6/350,978
PRIOR PILING DATE: 2002-01-25
PRIOR PLING DATE: 2001-11-05
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3298
LENGTH: 379
                                                                                                                                                                                                                                                                                                                            APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/11132142; Publication No. US20050276818A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.3
SEQ ID NO 7
                                                                               KAMAMOTO, JUN-ICHI
ISONO, YUUKO
110, YURI
                                                                                                                                                                                                                                                                     YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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; ORGANISM: Saccharomyces sp.
US-11-132-142-7
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Best Local Similarity 100.
                                                              SHIZUKO
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NAGAI, KEIICHI
                                                                                                                                                                                                                                               SEKI, NAOHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 EYFDSL 168
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TITLE OF INVENTION: NUCLEIC ACID AND POLYBERTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REPERRENCE: 09531-12801
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT PELLING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR APPLICATION NUMBER: DC $6/416,395
PRIOR APPLICATION NUMBER: US $60/416,395
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 10357
                                                                                                                                                                                                           APPLICANT: Stratagene California
APPLICANT: Stratagene California
TITLE OP INVENTION: Compositions And Methods For Reverse Transcription
FILE REPERENCE: 25436/2452
CURRENT APPLICATION NUMBER: US/11/100,183
CURRENT APPLICATION NUMBER: US 60/559,810
PRIOR PILING DATE: 2004-04-06
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.2
SEQ ID NO 37
LENGTH: 231
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Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches
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Publication No. US20060024696A1
GENERAL INFORMATION:
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Publication No. US20060029945A1
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ORGANISM: Lawsonia intracellularis
                                                                                                                                                    Sequence 37, Application US/11100183
Publication No. US20050272074A1
GENERAL INFORMATION:
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US-11-100-183-37
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APPLICANT: SUGIYAMA, TOMOYASU
                                           1814 ASVTNSV 1820
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43 ASVTNSV 49
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Sequence 1691, Application US/10821234
; Sequence 1691, Application US/2005025114A1
; Bequence 1691, Application No. US20050255114A1
; GENERAL INFORMATION:
    APPLICANT: Labat, Ivan
    APPLICANT: Labat, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
    TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT FILING DATE: 2003-04-07
; PRIOR PELING DATE: 2003-04-07
; PRIOR PELING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1691
; LENGTH: 766
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                                    Length 605;
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Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NOS: 12464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
11.8%; Score 6; DB 7;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches
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Pred. No. 59;
0; Mismatches
                                      11.8%; Score 6; DB 6; 100.0%; Pred. No. 49;
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US-11-072-512-3534
Sequence 3534, Application US/11072512
; Publication No. US20060029945A1
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100.0%; Pre
0; 1
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                   Ouery Match
Best Local Similarity 100..
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Best Local Similarity
Matches 6; Conserv
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US-11-087-099-5101
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US-10-689-742-140
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Sequence 140, Application US/10689742

Publication No. US20050250180A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: LaVallie, Edward R

APPLICANT: LaVallie, Edward R

APPLICANT: Tracky, User A

APPLICANT: Tracky, Maurice

APPLICANT: Spaulding, Vikki

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FILE REPRENCE: 0076.000091.10

CURRENT APPLICATION NUMBER: US/10/689, 742

CURRENT FILING DATE: 2003-10-22

PRIOR FILING DATE: 2003-12-21

NUMBER OF SEQ ID NOS: 231

SOFTWARE: Patentin version 3.2

SEQ ID NO. 14.0
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APPLICANT: IRLE, RYCTARO
APPLICANT: SEKI, NADHIKO
APPLICANT: SEKI, NADHIKO
APPLICANT: YOSHIKAN, TSUTOMU
APPLICANT: OTSUKA, MOTOVIKI
APPLICANT: OTSUKA, MOTOVIKI
APPLICANT: MAGNHO, YASUHIKO
ITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR PLING DATE: 2002-01-25
PRIOR FLING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VET. 201-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VET. 2.1
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                                  Sequence 3907, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISCGAI, TAKAO
APPLICANT: OTGINIA, TOMOYASU
APPLICANT: OTGINIA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: STOR
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Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                   NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                               OTSUKA, KAORU
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ORGANISM: Homo sapiens
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                            US-11-072-512-3907
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LENGTH: 605
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Gaps . ö

Gaps

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APPLICANT: SUGITAMA, TOMOYASU
APPLICANT: GUGITAMA, TOMOYASU
APPLICANT: GUSTAM, TOMOYASU
APPLICANT: GUSTAM, TESSUI
APPLICANT: SATO, HIROTOWI
APPLICANT: SHIZUKO
APPLICANT: SHIZUKO
APPLICANT: SHIZUKO
APPLICANT: SHIZUKO
APPLICANT: SHIZUKO
APPLICANT: GUSTAM, TESTONO
APPLICANT: GUSTAM, TESTONO
APPLICANT: GUSTAM, MOTOWIL
APPLICANT: GUSTAM, GUSTAM
APPLICANT: GUSTAM
APPLICANT
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Search completed: March 2, 2006, 04:42:39 Job time: 22 secs

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JS-09-565-423-11
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,026, A

50243, A

,e 28431, A

,uence 25925, A

,duence 19314, A

Sequence 19314, A

Sequence 4388, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Appl
Sequence 11115, A
Sequence 6, Appli
Sequence 9, Appli
Sequence 21, Appl
Sequence 7, Appli
Sequence 13, Appl
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
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Sequence 10, Appl
Sequence 60339, A
Sequence 5704, Ap
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2, Appli
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Sequence 26879, 2
Sequence 44871, 2
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91.662 Million cell updates/sec
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51
1 MLQMAGQCSQNEYFDSLLHA......TPPLTCQRYCNASVTNSVKG
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                                                                                                             Seconds
              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2_6/ptodatcal/iaa/5_COMB.pep:*

2: /cgn2_6/ptodatcal/iaa/f_COMB.pep:*

3: /cgn2_6/ptodatcal/iaa/H_COMB.pep:*

4: /cgn2_6/ptodatcal/iaa/HFCOMB.pep:*

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6: /cgn2_6/ptodatcal/iaa/RB_COMB.pep:*
                                                                                                             March 2, 2006, 04:27:47; Search time 46
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US-09-949-016-11115

US-09-854-864-5

US-09-854-864-2

US-09-854-864-2

US-09-854-864-12

US-09-854-864-12

US-09-854-864-12

US-09-854-864-12

US-09-854-864-12

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US-09-854-864-11

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US-09-854-864-11

US-09-854-864-11

US-09-854-864-11

US-09-21-976-5704

US-09-210-252-2

US-09-210-252-2

US-09-210-252-2

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US-09-210-252-2

US-09-270-767-35026

US-09-270-767-35026

US-09-270-767-35026

US-09-270-767-35026

US-09-252-991A-23579

US-09-252-991A-23579

US-09-252-991A-23579

US-09-248-796A-19314

US-09-248-796A-14858

US-09-243-681A-4388
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                                                                               OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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28 6 11.8 291 2 US-09-198-452A-373 Sequence 373, App 29 6 11.8 291 2 US-09-438-185A-359 Sequence 15551, App 31 0 US-09-9438-185A-359 Sequence 15551, App 31 0 US-09-902-540-15551 Sequence 15551, App 32 0.09-902-540-15551 Sequence 15551, App 32 0.09-902-540-15591 Sequence 15551, App 32 0 US-09-328-352-7098 Sequence 415, App 34 0 US-09-270-767-46598 Sequence 415, App 35 0 US-10-104-047-3298 Sequence 1558, App 35 0 US-10-104-047-3298 Sequence 58641, App 37 0 US-09-270-767-58641 Sequence 58641, App 37 0 US-09-270-767-588-10 Sequence 58641, App 37 0 US-09-487-5588-404 Sequence 511, App 40 0 US-09-487-5588-404 Sequence 276, App 41 6 US-09-902-540-9827 Sequence 15175, App 42 6 US-09-949-016-10424 Sequence 10424, App 44 6 US-09-949-016-10424 Sequence 10424, App 44 6 US-09-949-016-10424 Sequence 10424, App 44 6 US-09-949-016-10424 Sequence 10424, App 45 0 US-09-9490 US-0949-016-10424 Sequence 10424, App 45 0 US-09-9490 US-0949-016-10424 Sequence 10424, App 45 0 US-09-9490 US-09490 US-09490 US-09490 US-09490 US-09490 US-09490 US-09490 US-09490 US-0949
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#### ALIGNMENTS

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patent No. 647597

patent No. 647597

patent No. 647597

general Introduction US/09565423

patent No. 647597

general Introduction The Properties of Sequence 11, Application US/09565423

general Introduction Taill No. 967597

TITLE OF INVENTION: AMENDER: US/09/565,423

CURRENT PALCATION WUMBER: US/09/565,423

CURRENT PALCATION WUMBER: US/09/565,423

CURRENT PALCATION WUMBER: G/132,892

PRIOR PALICATION WUMBER: G/132,892

PRIOR PALICATION WUMBER: G/132,892

PROPER PALICATION UND WUMBER: G/132,892

PROPER PALICATION WUMBER: G/132,7768

PRIOR PALICATION WUMBER: G/2021,7768

PRIOR PALICATION WUMBER: G/2021,7768
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: TY, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERENCE: A-686B
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-05-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS HOBE
APPLICANT: TYU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERSENCE: A-686B
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
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     Length 181;
Query Match
94.1%; Score 48; DB 2; Length 181,
Best Local Similarity 100.0%; Pred. No. 2.3e-43;
Matches 48; Conservative 0; Mismatches 0; Indels
                                                                                                   4 MAGQCSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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86.3%; Score 44; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.6e-39;
Matches 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 44
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Patent No. 6774106
                                                                                                                                                                                                                                                                      ; Sequence 9, Application US/09854864
; Patent No. 6774106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
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SOFWARE: Patentin version 3.1
SEQ ID NO 9
LENCTH: 283
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Best Local Similarity 100.
Matches 48; Conservative
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US-09-854-864-21
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US-09-854-864-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: METHODS AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT APPLICATION NUMBER: US/09/1039
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EXDE
APPLICANT: THEILL, LARS EXDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR PLING DATE: 2000-06-17
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENT VERSION 3.1
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                                                                                                                                                                                                                                                                             1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                              9 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTFPLTCQRYCNASVTNSVKG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 48
                                                                                                                                                                               Score 51; DB 2; Length 192;
Pred. No. 1.6e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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94.1%; Score 48; DB
Best Local Similarity 100.0%; Pred. No. 7.9
Matches 48; Conservative 0; Mismatches
                                                                                                                                                                            Query Match
100.0%; Score 51; DB
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 51; Conservative 0; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11115
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EXDE
; APPLICANT: THEILL, LARS EXDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09854864
Patent No. 6774106
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CORGANISM: Homo sapiens
US-09-854-864-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                        ; ORGANISM: Human
US-09-949-016-11115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
LENGTH: 181
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US-09-854-864-5
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GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
                APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-6868
CURRENT APPLICATION NUMBER: US, 09/854,864
CURRENT PEDELICATION NUMBER: US, 06/204,039
PRIOR FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PLANG DATE: 2000-06-27
SEQ ID NO 12
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 2379-72
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR PELICATION NUMBER: 60/132,892
PRIOR PELICATION NUMBER: 60/132,892
PRIOR FILING DATE: 1999-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 185,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10; DB 2; Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                       19.6%; Scc...
100.0%; Pred. No. ...
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Patent No. 6774106
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Patent No. 6475987
                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: human-murine Consensus
LARS EYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Conservative
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US-09-565-423-17
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hes 10; Conserv
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Best Local Similarity
Matches 10; Conserv
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFRENCE: A-686B
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 13
                                                                                                                                                              APPLICANT: THEILL, LARS EXDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MAITER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
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Pred. No. 8.6e-29;
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100.0%; Pred. No. 4.1e-29;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                  FILE REPERENCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
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Patent No. 6774106
GENERAL INFORMATION:
                                                                                        nce 7, Application US/09854864
No. 6774106
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Matches 34; Conservative
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US-09-854-864-7
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ORGANISM: Consensus
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ઠે 셤 PRIOR APPLICATION NUMBER: US 60/204,039

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Sequence 2, Application US/09510252

| Sequence 2, Application US/09510252
| Patent No. 6372490
| GENERAL INFORMATION:
| APPLICANT: Nandabalan, Krishnan
| APPLICANT: Schulz, Vincent
| APPLICANT: CuraGen Corporation
| TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
| FILE REPREMENCE: 15966-524 MDM US
| CURRENT APPLICATION NUMBER: USN 60/121,192 |
| PRIOR APPLICATION NUMBER: USN 60/121,192 |
| PRIOR PLLING DATE: 1999-02-23 |
| PRIOR FILING DATE: 1999-02-23 |
| PRIOR FILING DATE: 1999-03-03 |
| NUMBER OF SEQ ID NOS: 4 |
| SOFTWARE: Patentin Ver. 2.0 |
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Length 29;
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11.8%; Score 6; DB 2;
100.0%; Pred. No. 19;
:ive 0; Mismatches
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   Query Match 11.8
Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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; LOCATION: -43..-1
US-09-621-976-5704
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Facult No. 6774106

GENERAL INFORMATION:
FARILL, LARS EYDE

APPLICANT: THEILL,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-6868

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-06-12

PRIOR FILING DATE: 2000-06-12

PRIOR FILING DATE: 2000-06-12

NUMBER OF SEQ ID NOS: 31

SOFTWARER: Patentin version 3.1

SEQ ID NO 10

LENGTH: 281
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 326-094
CURRENT APPLICATION NUMBER: 18/19/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60339
LENGTH: 29
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0.0075;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                             19.6%; Score 10; DB 2; Length 185; 100.0%; Pred. No. 0.0053; tive 0; Mismatches 0; Indels
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US-09-270-767-60339
   PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 185
TYPE: PRI
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Best Local Similarity 100.
Matches 10; Conservative
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; ORGANISM: Mus musculus
US-09-854-864-10
                                                                                                                                                                                                                                                       ORGANISM: Murine
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US-09-854-864-10
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Search completed: March 2, 2006, 04:29:06 Job time : 47 secs

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950 952 952 964 981 981 1000 1008 1115 1115 1418

ALIGNMENTS

gallus gall homo sapien mus musculu mus musculu

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Biocceleration Ltd.
GenCore version
Copyright (c) 1993 - 2006
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sw model protein search, using Run on:

March 2, 2006, 04:20:42; Search time 235 Seconds (without alignments) 153.115 Million cell updates/sec

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Onrigo Gapop 60.0 , Gapext 60.0 Scoringetablies

2166443 segs, 705528306 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to becore greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result No.	Score	Watch	Query Match Length	DB	QI	Description
-	51	100.0	184	-	TNR17 HUMAN	Q02223 homo sapien
8	51	100.0	184	N	Q6PE46 HUMAN	
m	10	19.6	185	ч	TNR17 MOUSE	_
4	8	15.7	148	~	QSJK76 ORYSA	oryz
2	∞	15.7	499	~	088714 MOUSE	mus
9	α	15.7	1674	7	Q80Z18 MOUSE	mus
7	80	15.7	2850	7	Q80T03 MOUSE	Q80t03 mus musculu
8	7	13.7	140	~	QB00M3_MORAM	morone
6	7	13.7	140	7	Q800M4 MORCH	morone
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1	7	13.7	140	~	Q800M6 MORSA	_
	7	13.7	175	~	QBBHX4 MOUSE	_
	7	13.7	202	~	Q9JDQ3_9HIV1	
	7	13.7	206	7	Q8LX76 9DIPT	-
15	7	13.7	207	7	Q8AS74_9HIV1	
16	7	13.7	258	7	Q8BHS1 MOUSE	
17	7	13.7	264	7	Q4YHA8_PLABE	
18	7	13.7	307	~	Q4YZ16_PLABE	
19	7	13.7	307	~	QSDIB6 EPICO	Osdib6 epinephelus
20	7	13.7	309	7	Q9WYY9_THEMA	-
21	7	13.7	333	7	Q678F3_9VIRU	
22	7	13.7	385	N	Q6MT77 MYCMS	_
23	7	13.7	409	~	Q672Q5_9HIV1	
24	7	13.7	411	~	QSFW06 XENTR	xeno
25	7	13.7		~	Q5U4G6_MOUSE	BUM
26	7	13.7		7	Q8K3A5_MOUSE	mus
27	7	13.7		7	Q8BHQ2_MOUSE	
28	7	13.7		7	Q4HZP5_GIBZE	gibberel
29	7	•		7	Q8AVS9_XENLA	٠.
30	7	13.7	œ	7	OBWRL8_TETTH	
31	7	13.7	945	7	Q52FS8_MAGGR	Q52f88 magnaporthe

## Best Available Copy

RESULT 1 TNR17 HUMAN ID TURI17 HUMAN STANDARD; PRT; 184 AA.	01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 13-SEP-2005 (Rel. 48, Last annotation update) Tumor nerrosis factor receptor superfamily member 17 (B-cell	maturation protein). Name-BTRERST17, Synonyms-BCM, BCMA; Name-BTRERST17, Synonyms-BCM, BCMA; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606;		424-44	UCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.592  Loftus B.J., Kim UJ., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deelattes Mays A., Cao Y., Xu R.X., Rang HL., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.; "Genome duplications and other features in 12 Mb of DNA sequent of the consone 16p and 16q."; Genomics 60:295-308(1999).  [4]. NUCLEOTIDE SEQUENCE, AND VARIANT THR-153. MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/63637 KAWASBAKI A., TBUChiya N., FUKAZAWA T., HABSHIMOLO H., TOKUNAS	"Presence of four major haplotypes in human BCMA gene: lack or association with systemic lupus erythematosus and rheumatoid arthritis.";  Genes Immun. 2:276-279(2001).  [5]  NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-54; VAL-65; VAL-75; ASN-81 AND SER-165.  Livingston R.J., Rader M.J., Chung MW., Ritchie T.K., Olson A.N., Manyon C P. Nanyon D.A. Poel C.L., Robertson P.D., Schackwitz W.S., Nanyon C P.
E CL	88223	800008 80008	R R R R R R R R R R R R R R R R R R R	8 2 2 2 2 L L L L	&	RA RE

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED sustantion the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;
Shu H.-B., Johnson H.
"B cell acturation protein is a receptor for the tumor necrosis factor family member TALL-1.";
Proc. Natl. Acad. Sci. U.S. A. 97:9156-9161(2000).
-!- FUNCTION: Receptor for TNFS713/BLyS/BAPF and TNFSF13/APRIL.
Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NP-kappa-B and JNK.
-!- SUBUNIT: Associates with TRAFI, TRAF2, TRAF3, TRAF5 and TRAF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells or monocytes.

DISEASE: A chromosomal aberration involving TNFRSF17 is found in a form of T-cell acute lymphoblastic leukemia (T-ALL). Translocation t(4;16) (q26;p13) with ll2.
SIMILARITY: Contains 1 TNFR-Cys repeat.
Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.; "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)."; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.
MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
"APRIL and TALL-I and receptors BCWA and TACI: system for regulating
                                                                                                                                          MEDLINE=20363816; PubMed=1093733;
Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,
Inoue J.-I., Devergne O., Tampis A.;
"TNF receptor family member Edwa (B cell maturation) associates with
TNF receptor-associated factor (TRAF) 1, TRARZ, and TRAF3 and
activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-
ivated protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                          WEDLING=20259066; PubMed=10801128; DOI=10.1038/35010115; Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R., Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C., Moore M., Littau A., Grossaman A., Haugen H., Foley K., Blumberg H., Harrison K., Kindsvogel W., Clegg C.H.; "TACI and BCMA are receptors for a TNF homologue implicated in B-cell autoimmune disease."; Nature 404:995-999(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9Y275:TNFSF13B; NDExp=1; IntAct=EBI-519945, EBI-519169;
--- SUBCELLIULAR LOCATION: Type III membrane protein. Plasma membrane and perinuclear Golgi-like structures.
--- IISSUB SPECIFICITY: Expressed in mature B-cells, but not in T-
                                                                                                                               FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z14954; CAA78679.1; -; mRNA.

EMBL; Z29575; CAA82691.1; -; mRNA.

EMBL; Z29574; CAA82690.1; -; Genomic DNA.

EMBL; U95742; AAB67251.1; -; Genomic DNA.

EMBL; BAS52772; BAB60895.1; -; Genomic DNA.

EMBL; AX509112; AAR84240.1; -; Genomic DNA.
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PDB; 1XU2; X-ray; R/S/T=5-51.
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HGNC; HGNC:11913; TNFRSF17.
                                                                                                                                                                                                                                                                                                                             Immunol. 165:1322-1330(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nat. Immunol. 1:252-256(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S43486; S43486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  humoral immunity."
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Ensembl; ENSG0
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MIM; 109545; -.
GO; GO:001621; C:integral to membrane; TAS.
GO; GO:0006886; C:plasma membrane; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0001275; P:development; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR001368; TNFR C6; FALSE NEG.
PROSITE; PSO:0652; TNFR NGFR 1; FALSE NEG.
3D-structure; Chromosomal translocation; Immune response;
POLYMORDHISM; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.
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Signal-anchor for type III membrane
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amnotation update)
Tumor necrosis factor receptor superfamily, member 17.
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5 -> N (in dbSNP:373496).
/FTId=VAR_018758.
                                                                                                                                                                                                                                                                                                                                        Cytoplasmic (Potential) TNFR-Cys.
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/FTId=VAR 018759.
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By similarity.
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Q6PE46;
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/c; TISSUB-Spleen;
MEDIATR=99061155; PubMed=904699; DOI=10.1093/intimm/10.11.1693;
MAGTY C., Laabi Y., CubMed=904619; Roussel J., Hatzoglou A.,
Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
The characterization of murine BCMA gene defines it as a new member of the tumor necrosis factor receptor superfamily.";
                                                                                                                                                                                                                                                                                                                                Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last amontation update)
Tumor necrosis factor receptor superfamily member 17 (B-cell
                                                                                                                                                                                                                                                                                                 Length 184;
                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                          Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC058291; AAH58291.1; -; mRNA. GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                      20139 MW; C7ACF9B40FC5531A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                 Score 51; DB 2; I Pred. No. 3.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 AA
                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Name=Tnfrsf17; Synonyms=Bcm, Bcma;
                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                       and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                Best Local Similarity 100. Matches 51; Conservative
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                                                                                                                                                                                                                                                                       184 AA;
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RY NUCLEOTIDE SEQUENCE LLANGE SCALLS MEANAL (ISOFORM 1).

RY NUCLEOTIDE SEQUENCE LLANGE SCALLS MEANAL (ISOFORM 1).

RY STEALNE-273BL/6J; TISSUE-Mammary gland;

REAL SEQUENCE T. Feingold E.A., Grouse L.H., Derge J.G.,

RA Attausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RAD Diatchenko L., Marushna K., Farmer A.A., Rubin G.M., Hong L.,

RAD SEADJeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RAD S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RAD S.S., McDan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RAD S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RICHARGS S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RICHARGS S., Worley K.C., Shevchenko Y., Bouffard G.G.,

RAD Willalon D.K., Muzny D.M., Sodergren B.J., Dickson M.C.,

RAD Willalon D.K., Muzny A.C., Shevchenko Y., Bouffard G.G.,

RAD Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

RAD Rodriguez A.C., Grimwood J.S., Schwutz J., Myers R.M.,

RAD RODRIGUEZ A.C., Grimwood J.S., Schwutz J., Myers R.M.,

RAD RODRIGUEZ A.C., Grimwood J., Schwutz J., Myers R.M.,

RAD RODRIGUEZ A.C., Grimwood J.S., Sharke M.A.,

RAD RODRIGUEZ A.C., Grimwood J.S., Jones S.J.M., Marra M.A.;

RAD RODRIGUEZ A.C., Grimwood J.S., Jones S.J.M., Marra M.A.;

RODRIGUEZ A.C., Grimwood J.S., Jones S.J.M., Rarra M.A.;

RODRIGUEZ A.C., Grimwood J.S., Solubys a role in the regularity).

PROMOTES B-Cell survival and plays a role in the regularity).

L. SUBNIT: Associates with TRAPI, TRAPIS TRAPIS AND TRAPIBLIC AND TRAPIBLIC TARRES AND TRAPIBLIC TARRES AN
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Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Alzawa K., Arakwa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Saaski D., Shibata K., Shinagawa I., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Ranalysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insoid=088472-2; Sequence=VSP_006507;
TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
heart, and at lower levels in kidney and lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane
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EMBL; AK020247; BAB32038.1; -; mRNA.

EMBL; BC027519; AAH27519.1; -; mRNA.

HSSP; Q02223; JODD.

Ensembl; ENSMUSGO000022496; Mus musculus.

MGI; MGI:1343050; Thfrsf17.

GO; GO:0016021; C:integral to membrane; TAS.

InterPro; IPRO01368; TNFR c6.

PROSITE; PS00652; TMPR GFR 1; FALSE NEG.

PROSITE; PS00650; TNFR NGFR 1; FALSE NEG.

Alternative splicing; Immune response; Receptor; Signal-anchor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 420:563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462
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TISSUE=Stomach
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NON TER
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REMBL; APO04225; BADB8061.1; -; Genomic_DNA.
REMBL; APO04225; BADB8061.1; -; Genomic_DNA.
REMBL; APO04225; ZINC_PROTEASE; UNKNOWN_I.
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                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eppermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein OSJNBa0024F24.16 (Hypothetical protein B1156H12.31).
                                                                                                                                                                                                                                                     19.6%; Score 10; DB 1; Length 185; 100.0%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 148;
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148 AA; 16215 MW; DB06C14D76E647CE CRC64;
                    Cytoplasmic (Potential).
TNFR-CyP
By similarity.
By similarity.
By similarity.
Missing (in isoform 2).
/FTIG-VSP_006507.
                                                                                                                                                                                                   8806352B4FD26A8E CRC64;
     protein (Potential)
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100.0%; Pred. No. 1.7;
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=OSJNBa0024F24.16; Synonyms=B1156H12.31;
                                                                                                                                                                                                                                                                  100.0%; Prec. ....
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088714 MOUSE
1D 088714 MOUSE PRELIMINARY; PRT;
AC 088714 7
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                      20442 MW;
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QSJK76;
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                           12 EYFDSLLHAC 21
                                                                                                                                                                                                                                                                                                                                                                                                          9 EYFDSLLHAC 18
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SEQUENCE 14
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COSJK76 OR

COSJK76 OR

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DT 10
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
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Broande F., Buisine M.P.;

Biochim. Biophys. Acta 1676:240-250 (2004).

Biochim. Biophys. Acta 1676:240-250 (2004).

EMBL; AJ511867; CAD54415.1; -; Genomic DNA.

EMBL; AJ511868; CAD54415.1; JOINED; Genomic DNA.

HSSP; O46162; IKO.

MGI; MGI:2663233; Muc6.

InterPro; IPR002919; Prot Inh_CR_TIL.

InterPro; IPR002919; Prot Inh_CR_TIL.

Pfam; PF0019846; VWF_D.

Pfam; PF001984; VWD; 3.

SMART; SM00216; VWD; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomasetto C.L.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJO10752; CRA09343.1; -; mRNA.
HSSP; P56682; ICCV.
Ensembl; ENSMUSGO000048191; Mus musculus.
MGI; MGI: 2663233; Muc6.
InterPro; IPR002919; Prot Inh_CR_TIL.
InterPro; IPR001846; VWP_D.
Pfam; PF01056; IIL; 1..
Pfam; PF010594; VWD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 499 MW; 04F89EF4F23EE61E CRC64;
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Last sequence update)
Last annotation update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Gastric mucin-like protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.7%; Score 8; DB 2; 100.0%; Pred. No. 5.1;
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                                                                                                                        Name=Muc6; Synonyms=gastric mucin-like;
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AC 080218 MOUSE OF TERMILE1. 24,

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DT 01-JUN-2003 (TTERMILE1. 26,

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Best Local Similarity luversetive
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                                                                                                                                                             Mus musculus (Mouse)
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103 MLQMAGQ 109
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NON TER
NON TER
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22563400; PubMed=12676567; DOI=10.1016/S0888-7543(03)00036-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei; Moronidae; Morone.
NCBI_TaxID=46260;
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desseyn J.-L., Laine A.;

"Characterization of mouse muc6 and evidence of conservation of the gel-forming mucin gene cluster between human and mouse.";

gel-forming ma.433-436(2003).

EMBL; AY184388; AA047735.1; -; Genomic DNA.

EMBL; AY184386; AA047735.1; JOINED; Genomic_DNA.

EMBL; AY184386; AA047735.1; JOINED; Genomic_DNA.

EMBL; AY184386; AA047735.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleoste
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                                       Length 1674;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300398 MW; 9CD95F0845C79C9D CRC64;
 181168 MW; 3BC42CB004476309 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Insulin-like growth factor I receptor (Fragment).
Morone americana (White perch)
                                                                                                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.7%; Score 8; DB 2;
100.0%; Pred. No. 24;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AA.
                                       DB 2;
5. 15;
                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; O46162; 1KJO.
Ensembl; ENSMUSGO0000048191; Mus musculus
MGI; MGI:2663233; Muc6.
                                       Score 8; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro; IPR006207; Cys knot C.
InterPro; IPR002919; Prot Inh_CR_TIL.
InterPro; IPR001846; VWF D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                           Created)
                                       15.7%; (
100.0%;
                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, MAR-2004 (TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Query Match

Best Local Similarity luv...

Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBOOM3_MORAM PRELIMINARY;
                                                                                                                                                                                                                                                       Q80T03 MOUSE PRELIMINARY;
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fam; PF01826; TIL; 2.
fam; PF00094; VWD; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01225; CTCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1222 CSQNEYFD 1229
                                                                                                                                                        1181 ČŠÓNEYFĎ 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                              Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CSQNEYFD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2850 AA;
                                                                                                                  8 CSQNEYFD 15
                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                   Query Match
Best Local Similarity
     1674 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                        Name=Muc6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORAM
                                                                                                                                                                                                                                     MOUSE
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                                                                                                                                                                                                                  RESULT 7
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Fruchtman S., Hawkins M.B., Borski R.J.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of MPF (By similarity).
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Plays a key role in the control of the eukaryotic cell
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mitosis. Component of the kinase complex that phosphorylates the
repetitive C-terminus of RNA polymerase II. Catalytic component of
                                                                                                                                                                                                                                          -:- SUBMIT: Forms a stable but non-covalent complex with cyclin B in mature occytes (By similarity).

EMBL: AF402676; AA073861.1; -; mRNA.

HSSP; P08069; 1JQH.

SMR; Q800M3; 1-140.
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L; AF402675; AA073860.1; -; mRNA.
P; P08069; 1JQH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
1nsulin-like growth factor I receptor (Fragment).
Morone chrysops (White bass).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Buteleostei;
Actinopterygii; Neopterygii; Pelostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
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HISSP; P08065; 100H.
SMR; O800M4; 1-140.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
HITCHPROSITED SPROGENER TOTAL KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:ATP binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0016740; F:receptor activity; IEA.
GO; GO:0016740; F:rensferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00119; Prot kinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR0010946; Tyr pkinase.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 140;
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140 140
140 AA; 15787 MW; BB1B2C98A17E541B CRC64;
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Pred. No. 20;
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.7%;
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                                                                                                                                                                                                                              MPF (By similarity)
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103 MLQMAGQ 109
                                                                                                                                                                                                                                                                                                                                                    [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                      Moronidae; Morone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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SEQUENCE
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                                                                                            Q800M6
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Matches
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Plays a key role in the control of the eukaryotic cell cycle. It is required in higher cells for entry into S-phase and mitosis. Component of the kinase complex that phosphorylates the repetitive C-terminus of RNA polymerase II. Catalytic component of MPF (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in mature occytes (By similarity).
EMBL; AF402674; AA073859.1; -; mRNA.
HSSP; P08069; 1JQH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
11-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
11-SULIA-Like growth factor I receptor (Pragment).
Morone chrysops x Morone saxatilis (White bass x Striped bass).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
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GO; GO: 0004713; F.Protein-tyrosine kinase activity; IEA.
GO; GO: 0004872; F.receptor activity; IEA.
GO; GO: 0016740; F.transferase activity; IEA.
GO; GO: 0016740; F.transferase activity; IEA.
GO; GO: 1016740; F.transferase.
InterPro; IPR001719; Prot kinase.
InterPro; IPR001245; Tyr Dkinase.
InterPro; IPR001245; Tyr Dkinase.
InterPro; IPR001245; Tyr Dkinase.
InterPro; IPR001245; Tyr Dkinase.
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                                                                                                                                                                                                                                                       DB 2; Length 140;
                                                                                                                                                                                                                                                                                                      Indels
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140 140
140 AA; 15815 MW; AC3C1C98A1674D1B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%; Score 7; DB 2;
100.0%; Pred. No. 20;
iive 0; Mismatches
                                                                                                                                                                                                                                                                               ; Pred. No. 20;
0; Mismatches
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                       13.7%; Score 7; D
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Q800MS;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                            Local Similarity 100.
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                                                                                                                                         Receptor.
NON TER
NON TER
SEQUENCE
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                            Query Match
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Matches
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       STTABBATTS
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Name=Wdr12; Synonyms=AA959934;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus of day neonate head cDNA, RIKEN full-length enriched
library, clone:4831418P03 product:HYPOTHETICAL 28.4 KDa PROTEIN
homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mature ocytes (By similarity).

EMEL; AF402673; AA073858.1; -; mRNA.

EMEL; AF402673; AA073858.1; -; mRNA.

EMEL; AF402673; AA073858.1; -; mRNA.

SNR; Q800M6; 1-140.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0016740; F:ransferase activity; IEA.

GO; GO:00169; F:ransferase activity; IEA.

REINTS; PRO0109; PROTEIN_KINASE DOM; 1.

PROSITE; PSC00109; PROTEIN_KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 140 140 140 140 AA; 15787 MW; BB1B2C98A17E541B CRC64;
                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUAR-2004 (TrEMBLrel. 26, Last annotation update)
Insulin-like growth factor I receptor (Fragment).
Morone saxatilis (Striped bass).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
  140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.7%; Score 7; DB 2
100.0%; Pred. No. 20;
tive 0; Mismatches
PRT;
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QBBHX4;
  Q800M6 MORSA PRELIMINARY;
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nes 7; Conservative
                                                 01-JUN-2003 (TrEMBLrel. 01-JUN-2003 (TrEMBLrel.
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NUCLEOTIDE SEQUENCE
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QBBIX4 MOU
1D QBBIX
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DT 01-MA
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DE Mus m
DE 1ibra
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DE Name
OC Mus m
OC Muroi
OX NCEI
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NON TER
SEQUENCE
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Q9JDQ3_9HI
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Hukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiroka T., Kisukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Salto R., Saitoh H., Sakai C., Sakai K., Sakauki Y.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/6J; TISSUB-Head; MEDLINB-20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINB-20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                     MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=C7. Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Takiyama J., Nishi K., Kiteunai T., Tashinco H., Harada M., Sunin N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Yoneda Y., Inoue K., Togawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-134-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.; "Punctional annotation of a full-length mouse cDNA collection.";
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Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Head;
The FANTOM Consortium,
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"Consistent viral evolutionary changes associated with the progression of human immunodeficiency virus type 1 infection.";
J. Virol. 73:10489-10502(1999).

EMBL; AF137741; AAF31608.1; -; Genomic_RNA.

SMR; Q9JDQ3; 1-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20027278; PubMed-10559367;
Shankarappa R., Margolick J.B., Gange S.J., Rodrigo A.G., Upchurch D.,
Parzadegan H., Gupta P., Rinaldo C.R., Learn G.H., He X., Huang X.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses, Retro-transcribing viruses, Retroviridae, Orthoretrovirinae, Lentivirus, Primate lentivirus group.
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Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO76417; BAC36330.1; -; mRNA.
Ensembl; ENSMUGG00000035572; Mus musculus.
MGI; MGI:2140179; AM559934.
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                                                                                                                                                                                                                                                                     SEQUENCE 175 AA; 19571 MW; D5A62E8785D9F10F CRC64;
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Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. 28;
tive 0; Mismatches
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100.0%; Pred. No. 25;
ive 0; Mismatches
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                                                                                                                                                    InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 1.
SMART; SM00320; WD40; 1.
Hypothetical protein.
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QGJDQ3;
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Best Local Similarity 100...
7; Conservative
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                                         Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Chaoboridae;
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Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Lentivirus; Primate lentivirus group.
NCBI_TaxID=11676;
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Wang Y., Frey S., Gupta P., Learn G.H., Mittler J., Shriner D.,

Nickle D.C., Jennen M.A., Rodrigo A.G., Beerli P., He X., Zhao H.,

Rossini A., Felsenstein J., Walker B.D., Mullins J.I.;

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF555413, AAN07372.1; -; Genomic_RNA.

SMR, Q8AS74; 1-GO.
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13.7%; Score 7; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels
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13.7%; Score 7; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                   Berendonk T.U.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ427618; CAD4504.1; -; Genomic_DNA.
GO, GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
NOW TER
1 1
SEQÜENCE 206 AA; 23927 MW; E6BC8651EA8AE571 CRC64;
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207 AA; 22946 MW; DCD2182D0A73F90B CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
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09AS74 9HIV1 PRELIMINARY;
AC 0GAS74;
DT 01-MRR-2003 (TrEMBLrel. 23,
DT 01-MRR-2003 (TrEMBLrel. 23,
DT 01-MRR-2003 (TrEMBLrel. 23,
DT 01-MRR-2003 (TrEMBLrel. 24,
DE Envelope glycoprotein (Fragm
GN Name-env;
OS Human immunodeficiency virus
OC Viruses; Retro-transcribing
OC Viruses; Retro-transcribing
OC Lentivirus; Primate lentivir
OX NCBI TaxID=11676;
RN NCLEOTIDE SEQUENCE.
RA Wang Y., Frey S., Gupta P.,
RA Wang Y., Frey S., Gupta P.,
RA NOSSIMI A., Felsenstein J.,
RA ROSSIMI A., Felsenstein J.,
RL Submitted (AUG-2002) to the
DR SMR; OSA54; 1-207.
DR GO; GO:0016031; C:virtegral t
DR GO; GO:0016031; C:virtal enve
DR GO; GO:0016031; C:virtal enve
DR GO; GO:016031; C:virtal enve
DR GO; GO:016031; C:virtal enve
DR GO; GO:016031; C:virtal enve
DR Fam; PRO0516; GF120; 1.
KW AIDS; Envelope protein; Tran
FT NON TER 207 207
Chaoborus americanus.
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                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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                                                                                                          NCBI_TaxID=204565;
                        Mitochondrion.
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